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Abstract

The objective of this paper is to study forest growth simulation based on functional-structural modelling and its potentials for forestry applications. The GreenLab model is used for this purpose owing to its computational performances, its calibration capacity on real plants and its extension to the stand level, by taking into account the competition between neighbouring plants and the interactions with the environment.
We first propose a software design:

- *to manage the composition of forest scenes,*
- *to simulate their growth based on parallel computing of individual trees with the GreenLab model,*
- *to get the realistic and real-time 3D rendering of the simulation results.*

We then detail a test case to illustrate the potentialities of this new tool. Mono-specific stands of poplars and pines are simulated. We analyze the computation performances and illustrate the simulation results with 3D outputs. A very classical application in forest management, stand thinning, is also tested. Our tool provides new insights thanks to the detailed architectures of trees resulting from the functional-structural model.

1. Introduction

In 1975, Mitchell [1] had already foreseen the importance of simulation techniques to study the evolution of forest systems and their "response to initial spacing, thinning, genetic selection, fertilization, damages…". For this purpose, individual-based models were presented as the most promising means of study, as they were more detailed and faithful to reality than whole-stand models, despite their computational load. Since then, a lot of research efforts and of technological progresses have been made, which allows considering new prospects for forest growth simulation and management based on the fine description of interacting individuals. This paper aims at proposing an integrative synthesis of recent sciences and technologies, from individual-based modelling to efficient and realistic 3D visualization of forest functional growth.

Today, there already exist several sophisticated simulation platforms dedicated to forest management, with applicative tools. The usual strategy is to build a software around a given model to centralize developments, reuse components and methods, see for example SILVA, [2]. A more flexible possibility is an open software design, allowing various kinds of models to share the same simulation kernel and applicative tools, as proposed by Capsis [3]. So far, these platforms are mainly dedicated to empirical models, whose main drawback is their very specific scope in terms of environmental conditions and stand structures, which makes their predictive abilities limited outside their calibration database [4]. Despite this limitation, it seems that they are the only operational models for applications until today.

However, recent progresses in the development of (more) mechanistic individual-based models, describing the interactions between plants and with the environment may provide an alternative approach. One of the key works in this prospect is that of Sorrensen-Cothern *et al.* [5], which may be seen as the first functional-structural model (that is to say combining both functional growth processes and structural development, [6]), at stand level. More recent approaches are proposed for the GreenLab model [7], the LIGNUM model [8] and in the modelling environment GroIMP [9]. In [10], Pretzsch expressed his doubts about how detailed functional structural models could be used at forest scale, observing that such simulations concerned "only a few trees" so far. However, new mathematical formalisms like the structural factorization of trees [11] drastically reduces the computational load of functional-structural model simulation. Moreover, if the stand growth model allows considering

the interactions between plants and with the environment as inputs of each individual plant growth, then parallel computing can be used, which also opens new prospects in terms of simulation scale.

Finally, such simulation platforms dedicated to forest management could also benefit from the last advances in computer graphics to visualize large vegetation scenes in acceptable time (close to real time), with faithful representation of plant structure and functioning [12], [13], [14]. It is important to note that for ecosystem management, this faithful representation of both structure and functioning is the real objective, contrary to previous works in computer graphics implementing competition between plants in a stand but with the main objective of getting good looking images [15], [16].

The objective of our work is to study the potential uses for forestry applications of a functional-structural model - the GreenLab model - taking into account the interactions between plants and with the environment [17]. We first propose a software design:

- to manage the composition of forest scenes,
- to simulate their growth based on parallel computing of individual trees with the GreenLab model,
- to get the realistic and real-time 3D rendering of the simulation results.

We then detail a test case to illustrate the potentialities of this new tool. Mono-specific stands of poplars and pines are simulated. We analyze the computation performances and illustrate the simulation results with 3D outputs. A very classical application in forest management, stand thinning, is also tested.

2. Concepts and Software Design

In [10], Pretzsch *et al.* describe the algorithmic sequence for predicting forest development. Inspired by this description, we propose a simulation software that is based on 5 interacting modules, as described in Figure 1: a scene manager, a scene structure analyzer, a forest simulation manager, an individual-based functional-structural simulator and a 3D visualization engine. In the following, the functions of these modules and their interactions are described in details.

2.1. Scene Manager

The Scene Manager (developed in Java) derives from the Capsis forest simulation platform [3], and is called Simeo. It provides an interactive user interface. We first suppose that the simulation starts from the beginning of the stand growth, that is to say from the emergence of the first trees. This hypothesis may seem a bit restrictive, but we will discuss later how to handle more general situations, with

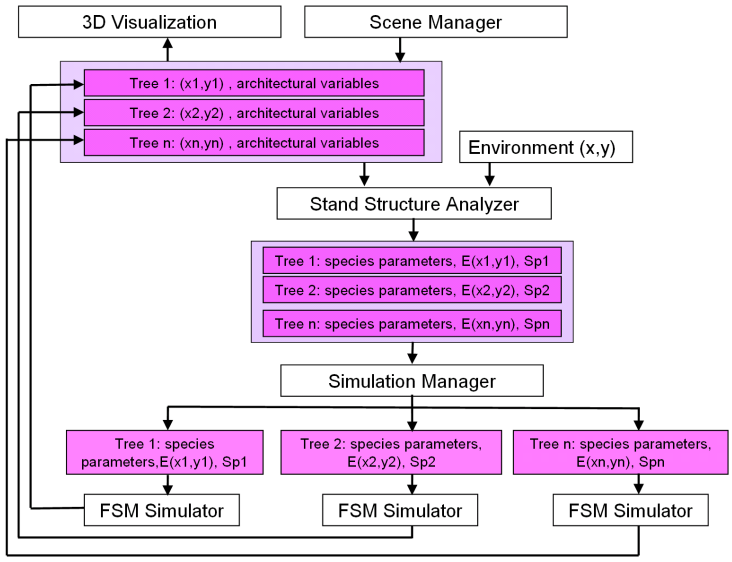

Figure 1. Software design. The first step is the input of data on the structure and site conditions of the monitored stand (Scene Manager and Environment Data); the second step is the analysis of the spatial stand structure which may particularly provide competition indices for each individual (Stand Structure Analyzer); the Simulation Manager may then dispatch all the individual simulations and run the Individual Functional-Structural Simulators independently; finally, all the architectural variables are available for a fine 3D representation of the stand (3D Visualization)

any initial conditions. The scene dimensions are chosen and its composition is specified in terms of population composition and positions of individuals. We can define a specific scene by giving the coordinates and species for each individual. However, in real situations, the exact spatial reparition is not generally available. Therefore, the scene manager proposes the generation of random scenes, obtained from probability distributions for the population composition and tree positions, or corresponding to a statistical description. Various tools are offered: perturbation around alignments, random positions, random composition with given proportions ...

Simeo offers an opened architecture and many other tools can be added as plugins. Moreover Simeo aims at providing a scene evolution framework based on the kernel of Capsis, but explicitly dedicated to 3D scenes and their evolutions. It is possible to simulate the scene changes over time, possibly with the emergence of new individuals in the population, mortality, thinning, with the objective of being able to simulate the whole forest management process.

2.2. Stand Structure Analyzer

Connected to the Scene Manager, the Stand Structure Analyzer aims at characterizing the plant population from a functional point of view. It is connected to an environmental

module giving the useful data for all individuals (temperature, light, soil hydric status ...) and it uses geometrical tools to analyze the spatial interactions between individual in order to characterize the effects of competitions, in relation to the functional model chosen.
Several types of approaches have been used to model competition in forest stands. First, neighbourhood models define an interaction radius around an individual plant and a competition index is computed from the number of plants in the neighbourhood (and their sizes), see for example [18]. Another approach consists in defining a 2D projection of the space potentially occupied by a plant onto a $x - y$ plane. Neighbors are plants having overlapping projection disks, and different methods can be derived to deduce the effects of competition, see [19]. Based on this method, [16] and [20] proposed models taking into account asymmetric competition. Likewise, a 3D zone of influence can be defined and interactions between these zones analyzed, [5], [2]. A last classical approach uses the Voronoi Tessellation to determine the area potentially available to a plant, see [21], [22]. To illustrate our work, we use this last method by computing for each individual i in the population its Voronoi cell area S_i^d, which will be used by the individual-based plant growth model.
Figure 2 illustrates the Voronoi tessellation on a particular stand generated with the scene manager. Note that the stand structure analyzer is integrated to the scene manager `Simeo`, which helps getting useful information on the scene straightforwardly when generating it.

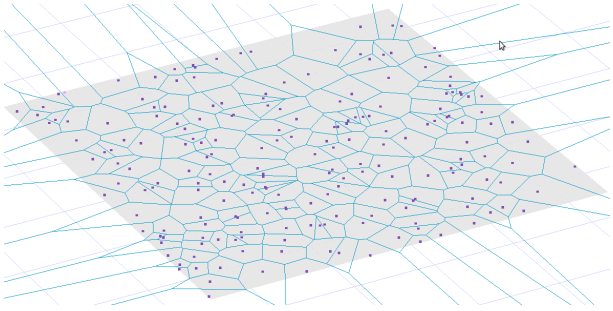

Figure 2. Voronoi tessellation of a stand

2.3. Simulation Manager

The objective of the Simulation Manager is to use the information given by the Stand Structure Analyzer to run the simulation of the whole stand growth. According to the evolution of the stand structure configuration, the simulation may be run for the whole simulation time (for example when only the Voronoi cell area is needed and if it stays constant across the simulation) or only for a time step when the simulation manager needs a regular update of the information regarding the stand structure (for example if architectures of the neighbouring plants are necessary to compute the interaction between individuals [20], since they vary across the simulation).
In order to take advantage of the technological breakthroughs regarding multiprocessors, multi-core computing, clusters or supercomputers, the Simulation Manager should be able to run the simulation of each individual independently of the others with parallel computing. For this purpose, we choose the `MPICH2` library (http://www.mcs.anl.gov/research/projects/mpich2/) which provides a widely-portable implementation of the Message Passing Interface (MPI) standard (http://www.mcs.anl.gov/research/projects/mpi/). MPI is well-adapted to handle our specific objective: the same program running with different sets of parameters (environmental conditions, neighbourhood configuration for competition, species ...) each corresponding to an individual plant.

2.4. An Individual-based Functional-Structural Model

The independent simulation of each individual tree in the plant stand is based on an individual-based functional structural model, taking into account competition between plants. Several types of models, with various ways to describe competition would fit in this framework. We use the GreenLab model of plant growth [17], which presents several advantages for this purpose:

- it describes plant growth at phytomer scale (internodes, leaves, fruits are precisely described);
- thanks to the powerful method of structural factorization presented in [11], the computation of both organogenesis and functioning is extremely efficient, even for trees of very complex architectures: the computation time is a linear or quadratic function of the simulation time, and is no longer proportional to the number of organs (which increases exponentially with the simulation time for trees);
- GreenLab models the retroactions of plant growth on organogenesis which allows the full expression of tree plasticity in competitive contexts [23];
- specific methods to estimate the parameters from experimental data were developed for trees [24];
- the effects of competition can be taken into account as inputs for each individual simulation [7], which is not the case for example when competition for light is modelled by computing light interception with radiosity techniques [25] or [9].

The GreenLab model of tree growth is described by a discrete dynamic system. The growth cycle generally corresponds to one year. Biomass production is computed according to Beer-Lambert's law [26] and to the environmental

conditions. Biomass is then allocated to the root system, to rings for the secondary growth and to buds for the new growth units. Accordingly, tree structure and architectural variables are updated between two growth cycles. We refer to [7] for a detailed presentation of the model and we simply recall here a simple and realistic way to take into account competition in the model.

For an individual tree, the biomass production at growth cycle n denoted $Q(n)$ is given by

$$Q(n) = E(n)\mu S_p(n)\left(1 - e^{-k\frac{S(n)}{S_p(n)}}\right)$$

where $E(n)$ is an environmental function at growth cycle n related to light radiation and to hydric stress, $S(n)$ is the tree leaf surface area, k is the extinction coefficient for Beer-Lambert's law, μ is the conversion efficiency and $S_p(n)$ is a characteristic surface area related to tree crown $x-y$ projection and to the space potentially available for tree development. As proposed in [7], $S_p(n)$ is given at growth cycle n by:

$$S_p(n) = \min\left[S_0\left(\frac{S(n)}{S_0}\right)^{\alpha}, S_d\right]$$

with S_0 and α two empirical coefficients estimated by model inversion from experimental data and S_d, the surface area of the Voronoi cell. $S_p(n)$ grows with the development of leaf surface and saturates at S_d. Such formulation is consistent with classical Beer-Lambert's law at field scale of process-based models, since at full cover we get that the production per m^2 is proportional to $\left(1 - e^{-kLAI(n)}\right)$ with $LAI(n)$ the leaf area index corresponding to the leaf surface area per m^2 [26].

2.5. 3D Visualization

The individual simulations provide the architectural and geometrical variables (at phytomer scale with GreenLab) of all the trees in the stand. It is thus possible to get a realistic 3D rendering of the forest. The simulator exports each tree using a high level format, consisting in an organ list with its associated location and orientations, on the basis of the AMAP technology presented in [27]. The single tree and scene rendering is performed by an OpenGl application, rendering, on the fly, a mesh representation of each tree organ. Simeo scene output is used to define each tree postition in the stand. Terrain texture mapping as well as sky and shadows are post processed, using classical computer graphics techniques.

Another tool aiming at real-time landscape visualization also uses the same export files (SLE, [28]). SLE is able to manage various vegetation layers like trees, shrubs, small plants, rocks, and other debris to complete the illusion of natural complexity. The individual tree files produced by the simulator are used to plant the forest and the spatialization of the other vegetation layers are defined by users. However, due to the real-time constraint, there is a limitation in the number of different polygon files that can be loaded simultaneously. Therefore, the Voronoi cell areas are gathered in classes (about 20), and a unique sample tree is chosen in each class for the geometrical representation.

3. Simulation of Mono-Specific Stands with Trees at Random Positions

We simulate the growth of two mono-specific stands of 50m×50m, with 200 trees of same ages and random positions in the stand. The first one is composed with 20 year old poplars and the second one with 30 year old pines.

3.1. Computation Performances

In Table 1 are shown the computation times with export of the polygon files and without. The forest growth simulation is run on a 2-processor workstation (each processor: quad core Intel© Xeon© E5420 2.5GHz) with OS Linux 2.6.27-11-generic Ubuntu. The standard performances (computations on one core) are compared to those obtained when using `MPICH2`, that is to say when taking advantage of the 8 cores to simultaneously run the simulation of 8 individual trees. We see that with `MPICH2` the computation is about 5 times faster than without. Moreover, we can observe that the geometrical export of polygon files is quite time-consuming compared to the computation of growth, especially for poplar trees that have very complex architectures with millions of organs to draw.

3.2. 3D Results

We present in Figure 3 and 4 the 3D visualization of the above mentioned poplar stand simulation, with 200 trees of same ages (20 years) and random positions in the stand. In Figure 3, different colors are used to represent trees from different classes of S_d and with the same colors, silhouettes of trees are shown (one individual in each class). Note however that if only 13 classes are represented, the growth of each individual tree was really simulated. The figure illustrates the differences in development of the trees according to the competition of their neighbours. These differences are detailed in Figure 5, in which 4 different poplars of the stand are represented, from the one enduring competition the most severely to the one growing in open field conditions. The differences in architectures result from the retroaction of functioning on organogenesis implemented in GreenLab [23]. More particularly, we can observe that the reiteration process only occurs when S_d exceeds $16m^2$.

20 year old poplar stand		
	Without 3D export	With 3D export
1 core	41.27 s	329.09 s
8 cores (MPICH2)	8.77 s	59.66 s
30 year old pine stand		
	Without 3D export	With 3D export
1 core	43.18 s	112.90 s
8 cores (MPICH2)	9.23 s	20.99 s

Table 1. Computation Performances for the Simulation of 200 Trees

3.3. Stand Thinning

With the Scene Manager, it is possible to simulate forestry scenarios, like thinning. This functionality derives from the one developed in the Capsis platform (see [29] for an example on thinning with Capsis). For the poplar stand considered above, we simulate the harvest of 100 trees out of 200 after 10 years. Note that we choose the harvested individuals randomly. The Stand Structure Analyzer provides the Voronoi cell areas before and after thinning, as illustrated in Figure 6.

Figure 7 shows the evolutions of stand biomass productions with and without thinning (note however that, even though realistic from a botanical point of view, the functional parameters used for the simulations do not correspond to a real calibration from experimental data). We see that after a severe decrease in biomass production due to thinning at year 10, the harvested stand catches up a part of the deficit to the reference stand. The density considered in our simulations are relatively low (800 individuals per ha). In case of high density, we should observe that after some time the production of the harvested stand reaches the level of the reference one. It opens perspectives in terms of harvest optimization.

4. Discussion

We have built a stand growth simulator with interesting properties for applicative and research purposes:

- it is based on a flexible and user-friendly interface allowing an easy management of the scene and of forestry scenarios;
- the forest stand simulation is based on individual-based models that can be run independently thanks to a preliminary analysis of the stand structure characterizing competition;
- the computation performances are excellent thanks

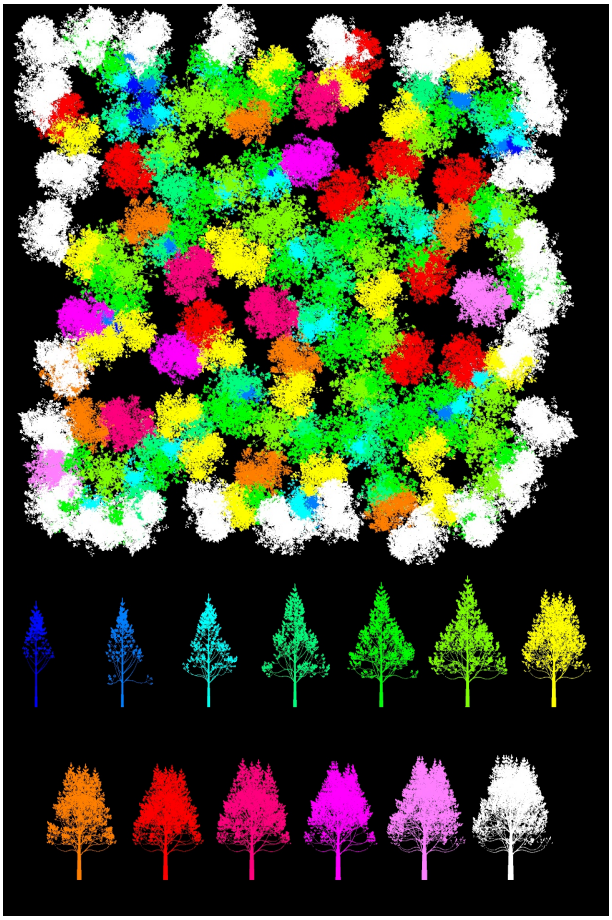

Figure 3. View of the stand from above with specific colours for each class of individuals according to their S_d , and the corresponding silhouettes for one individual in each of the 13 classes.

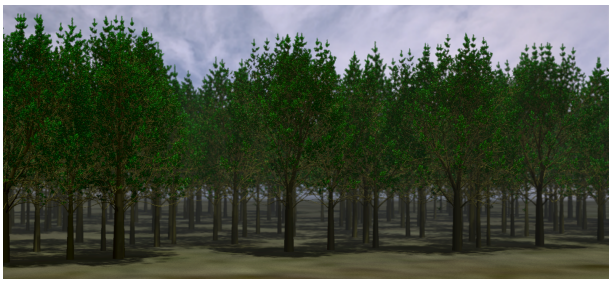

Figure 4. Pedestrian view of the forest

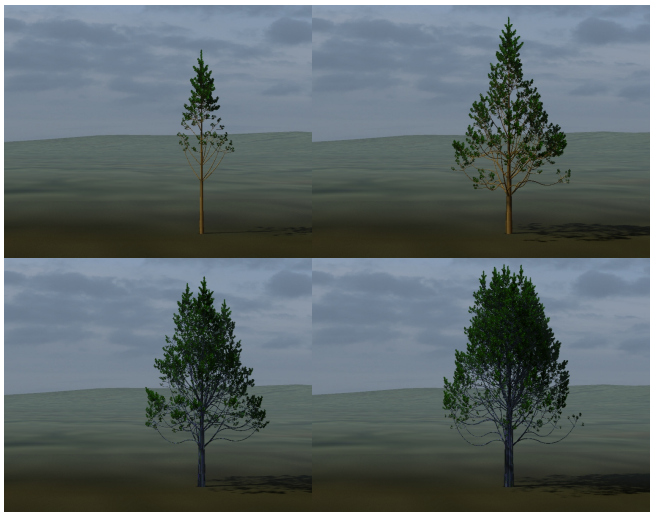

Figure 5. Isolated views of trees with $S_d = 3m^2,\ 10m^2,\ 20m^2,\ 40m^2$ in the poplar stand.

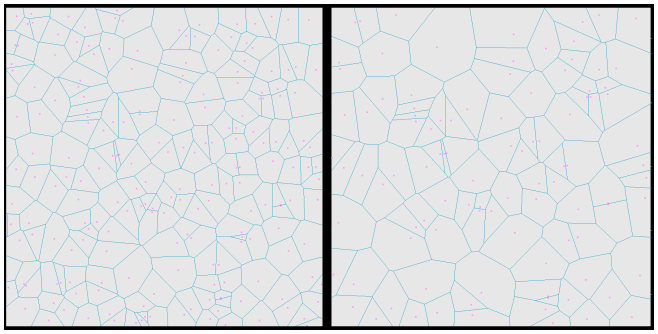

Figure 6. Voronoi tessellation before and after thinning

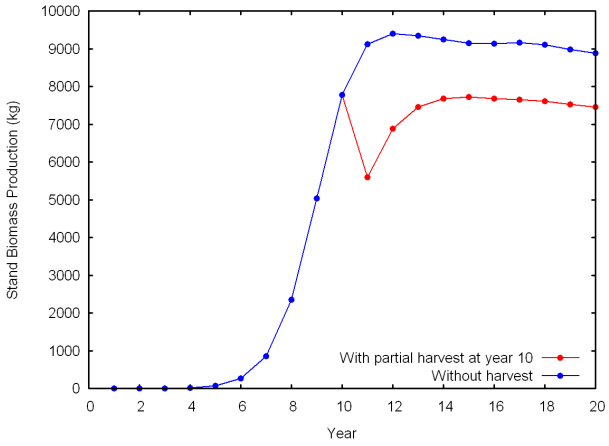

Figure 7. Annual stand biomass production with and without thinning

to the mathematical properties of the model chosen (GreenLab) and to the possibility of parallel computing, which opens perspectives in terms of optimization and calibration at stand level;

- a fine model of tree architecture (at phytomer level) and sophisticated 3D rendering provide new insights in stand description and understanding.

The test cases that we have presented concern mono-specific stands. Mixed forests could be simulated similarly, with different species at different ages. However, the Voronoi cell approach would be limited to handle inter-specific competition.

We have also simulated forest growth from the seed stage. This situation is realistic for cultivated stands or crops, but it would be interesting to be able to simulate a forest growth from any observed stage. It is theoretically possible, since the accurate knowledge of plant architecture at a given time is sufficient to predict its evolution. However, it would imply a very heavy description of each individual in the stand, which is prohibitive. Another approach based on data assimilation should also be possible, though not implemented yet: at time t_0, it would consist in guessing the tree history (for $t < t_0$) from a relatively low number of observations (by model inversion), thus be able to predict the evolution for $t > t_0$ and correct the prediction according to future observations.

Moreover, for long-term simulations, mortality should be incorporated in the growth model since it may affect significantly stand production. It is not properly modelled in GreenLab so far. Plant reproduction is not considered either. Other simulators introduced both aspects - mortality and reproduction - [16], based on simple hypotheses, for realistic simulations and graphical purposes. Such models could be implemented in the simulation framework that we propose. However, the biological mechanisms underlying mortality and reproduction remain poorly modelled. Improving this point is a promising perspective.

More generally, in order to be useful for applications in forestry, such simulations of stand growth should prove their predictive capacities, which is far beyond proposing realistic 3D rendering. The tool described in this paper does not have any predictive capacity yet. However, the frame seems well-adapted to develop this ability. Preliminary studies showed the possibility of calibrating the tree growth model GreenLab in different densities and environmental conditions [30], [24]. Assessing quantitatively the effects of competition from experimental data is currently under investigation.

Finally, modelling the interactions with the environment might lead to some difficult questions regarding competition for resources and synchronization of plant growth with the environmental submodels. These issues are those of functional landscape research [31] and a convergence of approaches should be considered in a near future.

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References

[1] K. Mitchell, "Dynamics and simulated yield of douglas-fir," *Forest Science (Monography 17)*, vol. 21, no. 4, p. 39p, 1975.

[2] H. Pretzsch, "The single tree-based stand simulator silva: construction, application and validation," *Forest Ecology and Management*, vol. 162, pp. 3–21, 2002.

[3] F. Coligny, "Efficient building of forestry modelling software with the Capsis methodology," in *Plant growth Modeling, simulation, visualization and their Applications.*, T. Fourcaud and X. Zhang, Eds. IEEE Computer Society (Los Alamitos, California), 2007, pp. 216–222.

[4] G. Mendoza and J. Vanclay, "Trends in forestry modelling," *CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources*, vol. 3, no. 10, 2008.

[5] K. Sorrensen-Cothern, E. Ford, and D. Sprugel, "A model of competition incorporating plasticity through modular foliage and crown development," *Ecological Monographs*, vol. 63, no. 3, pp. 277–304, 1993.

[6] R. Sievänen, E. Nikinmaa, P. Nygren, H. Ozier-Lafontaine, J. Perttunen, and H. Hakula, "Components of a functional-structural tree model," *Annals of Forest Sciences*, vol. 57, pp. 399–412, 2000.

[7] P.-H. Cournède, A. Mathieu, F. Houllier, D. Barthélémy, and P. de Reffye, "Computing competition for light in the GreenLab model of plant growth: a contribution to the study of the effects of density on resource acquisition and architectural development," *Annals of Botany*, vol. 101, no. 8, 2008.

[8] R. Sievänen, J. Perttunen, E. Nikinmaa, and P. Kaitaniemi, "Toward extension of a single tree functional-structural model of scots pine to stand level: effect of the canopy of randomly distributed, identical trees on development of tree structure," *Functional Plant Biology*, vol. 35, no. 10, pp. 964–975, 2008.

[9] R. Hemmerling, O. Kniemeyer, D. Lanwert, G. Buck-Sorlin, and W. Kurth, "The rule based language xl and the modeling environment gro imp illustrated with simulated tree competition," *Functional plant biology*, vol. 35, no. 10, pp. 739–750, 2008.

[10] H. Pretzsch, R. Grote, B. Reineking, T. Rötzer, and S. Seifert, "Models for forest ecosystem management: A european perspective," *Annals of Botany*, vol. 101, no. 8, pp. 1065–1087, 2008.

[11] P.-H. Cournède, M.-Z. Kang, A. Mathieu, J.-F. Barczi, H.-P. Yan, B.-G. Hu, and P. de Reffye, "Structural Factorization of Plants to Compute their Functional and Architectural Growth," *Simulation*, vol. 82, no. 7, pp. 427–438, 2006.

[12] P. Decaudin and F. Neyret, "Rendering forest scenes in real-time," in *Eurographics Symposium on Rendering*, J. Jensen and A. Keller, Eds. IEEE Computer Society (Los Alamitos, California), 2004.

[13] O. Deussen and B. Lintermann, *Digital Design of Nature - computer generated plants and organics*. Springer Verlag New York, 2005.

[14] X. Zhang, J. Liu, Z. Li, and M. Jaeger, "Volume decomposition and hierarchical skeletonization," in *VRCIA 2008 Conference, 8-9 December 2008. Biopolis, Singapour.*, A. Press, Ed. ACM Siggraph, December 8-9 2008.

[15] R. Mech and P. Prusinkiewicz, "Visual models of plant interacting with their environment," in *ACM SIGGRAPH'96 Proceedings*, 1996, pp. 397–410.

[16] M. Alsweis and O. Deussen, "Modeling and visualization of symmetric and asymmetric plant competition." in *Eurographics Workshop on Natural Phenomena*, E. Galin and P. Poulin, Eds., 2005.

[17] P. de Reffye, E. Heuvelink, D. Barthélémy, and P.-H. Cournède, "Plant growth models," in *Ecological Models. Vol. 4 of Encyclopedia of Ecology (5 volumes)*, S. Jorgensen and B. Fath, Eds. Elsevier (Oxford), 2008, pp. 2824–2837.

[18] E. Ford and K. Sorrensen-Cothern, "Theory and models of inter-plant competition as a spatial process," in *Individual-based Approaches in Ecology*, D. DeAngelis and L. Gross, Eds. Chapman and Hall, New York, 1992, pp. 363–407.

[19] G. Bonnan, "The size structure of theoretical plant populations: Spatial patterns and neighborhood effects," *Ecology*, vol. 69, no. 6, pp. 1721–1730, 1988.

[20] P.-H. Cournède and P. de Reffye, "A generalized poisson model to estimate inter-plant competition for light," in *Plant growth Modeling, simulation, visualization and their Applications.*, T. Fourcaud and X. Zhang, Eds. IEEE Computer Society (Los Alamitos, California), 2007.

[21] R. Mead, "A relationship between individual plant-spacing and yield," *Annals of Botany*, vol. 30, pp. 301–309, 1966.

[22] R. Daniels, H. Burkhart, and T. Clason, "A comparison of competition measures for predicting growth of loblolly pine trees," *Can. J. For. Res.*, vol. 16, no. 6, pp. 1230–1237, 1986.

[23] A. Mathieu, P.-H. Cournède, V. Letort, D. Barthélémy, and P. de Reffye, "A dynamic model of plant growth with interactions between development and functional mechanisms to study plant structural plasticity related to trophic competition," *Annals of Botany*, 2009.

[24] V. Letort, P.-H. Cournède, A. Mathieu, P. de Reffye, and T. Constant, "Parametric identification of a functional-structural tree growth model and application to beech trees (*Fagus sylvatica*)," *Functional Plant Biology*, vol. 35(10), pp. 951–963, 2008.

[25] G. Host, H. Stech, K. Lenz, K. Roskoski, and R. Mather, "Forest patch modeling: using high performance computing to simulate aboveground interactions among individual trees," *Functional Plant Biology*, vol. 35, no. 10, pp. 976–987, 2008.

[26] J. Vose, N. Sullivan, B. Clinton, and P. Bolstad, "Vertical leaf area distribution, light transmittance, and application of the beer-lambert law in four mature hardwood stands in the southern appalachians." *Canadian Journal of Forest Research*, vol. 25, pp. 1036–1043, 1995.

[27] M. Jaeger and P. de Reffye, "Basic concepts of computer simulation of plant growth," *Journal of Biosciences*, vol. 17, no. 3, pp. 275–291, September 1992.

[28] S. Griffon and D. Auclair, "Visualising changes in agricultural landscapes," in *Environmental and agricultural modelling: integrated approaches for policy impact assessment.*, F. Brouwer and M. Van Ittersum, Eds. Springer, 2009.

[29] A. Brin, C. Meredieu, D. Piou, H. Brustel, and H. Jactel, "Changes in quantitative patterns of dead wood in maritime pine plantations over time," *Forest Ecology and Management*, vol. 256, pp. 913–921, 1965.

[30] H. Guo, V. Letort, L. Hong, T. Fourcaud, P.-H. Cournède, Y. Lu, and P. de Reffye, "Adaptation of the greenlab model for analyzing sink-source relationships in chinese pine saplings." in *Plant growth Modeling, simulation, visualization and their Applications (PMA06).*, T. Fourcaud and X. Zhang, Eds. IEEE Computer Society (Los Alamitos, California), 2007.

[31] V. Le Chevalier, M. Jaeger, X. Mei, and P.-H. Cournède, "Simulation and visualisation of functional landscapes: effects of the water resource competition between plants," *Journal of computer science and technology*, vol. 22, no. 6, pp. 835–845, Nov. 2007.